AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0002] with the following amended paragraph:

[0002] The human diseases, the screening of the pathogenic genes and the functional research thereof are always important research fields. However, due to the systematic limitation, the possible living mechanisms are understood mostly through animal models which ~~are composed by~~ contain manipulated genes. For hundreds of years, *Drosophila Melanogaster* have been used as the basic source material for teaching and genetics study. In the last few decades, since the molecular biology method was brought into this field, the research of *Drosophila* molecular developmental genetics has entered into a new stage. The biological mechanism of *Drosophila* ~~has the feature of evolutional conservation~~ is very evolutionarily conserved. Therefore, from *Drosophila* study, people have come to understand ~~more about~~ that many human disease genes and cancer-related genes are derived from the gene mutation which controls the developmental mechanism. For example, the initiative mechanism of colon cancer and its complex working process are understood by studying the related genes of Wingless pathway which drives the development of abdominal segment formation in *Drosophila* embryo. Therefore, the main future studying direction of the present invention is doing the searching and studying of the specific functional genes in *Drosophila* genome based on the technique of the present invention. The *Drosophila* model will then be the base of searching the homologous genes of the human disease and pathogenic genes for the further study of human genetic mechanism.

Please replace paragraph [0003] with the following amended paragraph:

[0003] In the present time, as the ~~structure~~ structural genomic projects in model organisms are completed, how to decipher ~~the flood~~ a large amount of raw DNA sequences data in understanding gene function *in vivo* will be one of the major tasks for biology-related researchers. Different genomic strategies for defining and dissecting developmental and physiological pathways have been approached. The summit of these approaches is the systematic genomic screening of a specific functional trait using DNA tags such as P-transposon or retrovirus as mutagenesis agents. The designed transposon~~, as a mobile element,~~ can be used as a mobile element to rapidly obtain cellular

DNA sequence nearby the genetic mutation. The cellular DNA sequences can be obtained from the P-transposon-induced mutated genes loci by the direct use of inverse PCR (IPCR) or plasmid rescue methods. By such operating way, the inefficient and labor-intensive drill of cloning sequences for obtaining the junction sequence between the host and the mobile element can be circumvented. While retrovirus was used to mutate leukemia-causing genes in mouse (Li et al., 1999, Nature Genetics 23, 348), several hundred integration sites were cloned and characterized followed by high-throughput sequencing, data analysis and refined genetic mapping. Similarly, a global transposon mutagenesis in Mycoplasma allowed the question of the number of essential genes in a minimal genome to be answered (Hutchison, et al., 1999, Science 286, 2165). Therefore, by combining with emerging genomic tools, such systems in model organisms will indeed dramatically accelerate the pace of discovery in human disease-genes and cancer-related genes.

Please replace paragraph [0004] with the following amended paragraph:

[0004] For the functional study of *Drosophila* genes, a conventional approach relies on the creation of mosaic animals whereby the genotype varies in a cell-specific or tissue-specific manner. Currently, ~~almost~~ various techniques utilize the yeast FLP-FRT recombination system introduced into *Drosophila* (Golic and Lindquist, 1989, Cell 59, 499) to promote chromosomal site-specific exchange. This system allows the efficient recovery of homozygous patches in an otherwise heterozygous animal and thus permits a phenotypic analysis of mutant tissues.

Please replace paragraph [0005] with the following amended paragraph:

[0005] Different versions of the FLP-FRT (Flippase-Flippase Recombination Target sequence) system have been established for analyzing gene functions in either somatic or germline tissues. The direct mosaic productions in different somatic tissues have been established (Xu and Rubin, 1993, Development 117, 1223; Duffy et al., 1998, Development 125, 2263). In these methods, different tracing markers are used as the controls to monitor the presence of homozygous clones of genes to be studied. In addition, the FLP-DFS technique suitable for asking germline functions for loci ~~resided~~ residing in more than 95% of the genome has also been systematically completed (Chou and Perrimon, 1992, Genetics 131, 643; Chou et al., 1993, Development, 119, 1359 and Chou and

Perrimon, 1996, Genetics 144, 1673). The FLP-DFS technique uses the X-linked germline-dependent dominant female sterile mutation *ovo*^{D1} as a selection marker for the detection of germline recombination events. Nevertheless, the FLP-FRT system is used to promote site-specific chromosomal exchange (Chou and Perrimon, 1992, Genetics 131, 643).

Please replace paragraph [0006] with the following amended paragraph:

[0006] However, the major drawback for all of these FLP-FRT methods is that the mobile element such as the P-transposon can not be used directly as the mutagenesis agent to mutate the FRT chromosomes. While Δ2-3 transposase is recognizing the *P* transposon insertion as the mobilization origin, it simultaneously recognizes and transposes the *P[FRT]* insertions used in the FLP-FRT system. Under such situation, the genetic recombination cannot ~~be proceeded~~ proceed due to the fact that the *P[FRT]* chromosomes are not homologous. For example, the mobilized *P[FRT]* will mostly create a non-homologous condition. However, the germline recombination of *P[FRT]-ovo*^{D1} chromosome needs the existence of the homologous *P[FRT]* chromosome when *P[FRT]-ovo*^{D1} chromosome is used for the FLP-DFS germline recombination. Therefore, the transposition of the *P[FRT]* insertion results in a non-homologous condition so that the germline recombination cannot proceed ~~be proceeded~~.

Please replace paragraph [0007] with the following amended paragraph:

[0007] Presently, only ~~the EMS~~ EMS-based methods can be used for a full-scale genome-wide screening when using FRT chromosomes. Many interesting genes have been recovered. However, the goal to completely recover and to do molecular characterization of all interesting loci efficiently would be difficult if only ~~the EMS~~ EMS-based methods are ~~is~~ used for mutagenesis. Because ~~the~~ EMS produces mostly point mutations, it does not create any molecular tags on mutated genes for cloning manipulation. Consequently, the approach for identifying important genes is heavily impeded by the inefficient and labor-intensive traditional molecular cloning procedures.

Please replace paragraph [0008] with the following amended paragraph:

[0008] Another alternative strategy to facilitate gene cloning is to use transposition system independent of the P transposon. For example, the Hobo element system can be used to cause the gene mutation. However, the problem of creating a chromosomal environment ~~where to~~ that completely avoids the P transposon system has not been possible in the *Drosophila* field. This kind of approach has never been described in the field while the versatile FLP-FRT system has been publicized since 1989 (Golic and Lindquist, 1989, Cell 59, 499).

Please replace paragraph [0010] with the following amended paragraph:

[0010] In order to overcome the foresaid drawbacks, the present invention circumvents the above difficulties by constructing an advanced version of *P[FRT]* insertions on the *Drosophila* second chromosome, which allows the *P*-directed mutagenesis to ~~achieve purposes of~~ be useful for quick chromosome-wide screening and fast molecular cloning for the various FLP-FRT methods. Molecular biology technique such as inversed PCR (polymerase chain reaction) and plasmid rescue methods can be used to recover flanking genomic DNA sequences and relevant molecular properties of the genes affected by the transposon. Based on the mutated phenotypes of either germline or somatic recombinant clones produced, the biological functions can be described for the genes mutated. The integrated description of the molecular natures and biological functions of *Drosophila* genes can accelerate the understanding of the functions of human gene homologues and be used as the basis for the application and development of gene-based medicines.

Please replace paragraph [0080] with the following amended paragraph:

[0080] The primers used are defined by the 5' to 3' sequence base pair numbered in the FBtp0000348 locus, that is the *P[hsneo>>, ry^{+}, FRT]* element, and AE003781 genomic clones for *clipped P[hsneo>>, ry^{+}, FRT]^{40A}*, and in the FBtp0000268 locus, that is the *P[>w^{hs}>, FRT]* element, and AE003789 genomic clones for *clipped P[>w^{hs}>, FRT]^{42B}*.

Primers used for *clipped P[hsneo>>, ry^{+}, FRT]^{40A}* PCR reactions (SEQ ID NOS:12-25)

40SE	CGACGAGTTGCTTCTCCCACA	240516-240536 in AE003781 clone
40AS	GTTTCCCTCGCACTGCTATTT	240952-240932 in AE003781 clone
5'SE	CCGTCGAAAGCCGAAGCTTA	26-45 in FBtp0000348 locus
5'AS	CCCAAGGCTCTGCTCCCACAATT	254-232 in FBtp0000348 locus
ry1	CGCACGGTTTCAATCACA	948-930 in FBtp0000348 locus
ry2	GGTTACGAGGCAGCAGTTCTA	2070-2050 in FBtp0000348 locus
ry3	AACGCCCACTTCCGTATTGC	4035-4016 in FBtp0000348 locus
ry4	AATCCTGGTGCTTGCTTTCCT	6092-6072 in FBtp0000348 locus
Hsp	GTAGGTCATTTGTTTGGCA	8028-8046 in FBtp0000348 locus
neo	CTGATGCCGCCGTGTTC	8587-8603 in FBtp0000348 locus
FRTf	CCCCGCATGGAATGGGATAAT	9609-9629 and 10326-10346 in FBtp0000348 locus
FRTr	AGTCCGGTGCGTTTTT	9948-9933 and 10665-10650 in FBtp0000348 locus
3'SE	AAACCCCACGGACATGCTAA,	14861-14880 in FBtp0000348 locus
3'AS	CGGCAAGAGACATCCACTTA.	14993-14974 in FBtp0000348 locus

Primers used for *clipped P[>w^{hs}>, FRT]^{42B}* PCR reactions are listed below (SEQ ID NOS:12-25)

42SE	TGCTCGCTTGGATGAAC	11032-11047 in AE003789 clone
42AS	AGTGGAGTGGGAGTGGA	11600-11584 in AE003789 clone
5'SE	CCGTCGAAAGCCGAAGCTTA	26-45 in FBtp0000268 locus
5'AS	CCCAAGGCTCTGCTCCCACAATT	254-232 in FBtp0000268 locus
FRTf	CCCCGCATGGAATGGGATAAT	2549-2529 and 7937-7917 in FBtp0000268 locus
FRTr	AGTCCGGTGCGTTTTT	2210-2225 and 7598-7613 in FBtp0000268 locus
3'SE	AAACCCCACGGACATGCTAA	15101-15120 in FBtp0000268 locus
3'AS	CGGCAAGAGACATCCACTTA	15214-15233 in FBtp0000268 locus